SEQUENCE LISTING

<110> Genentech, Inc. Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.

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135

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<213> Homo sapiens
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<400> 23

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Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr $180 \,$ $185 \,$ 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr 195 200 205

<210> 24

<211> 28

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<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<220>
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<222> (21)
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<213> Homo sapiens
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ttaccatacg ccctcaggac gttccctcta gctggagttc tggacttcaa cagaacccca 180
tccagtcatt ttgattttgc tgtttatttt ttttttcttt ttctttttcc caccacattg 240
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caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140
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gaagctacac gcctccaact cctaccacat cgaaacttcc cacgattcct gactgggatg 1500
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cgtcccacag catgggctcc ccctttctgc tggcgggctt gatcgggggc gcggtgatat 1920
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Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
                         55
Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
                     70
                                          75
 65
Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
                                      90
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
                                                     110
            100
                                105
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Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala

120

115

- Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser 130 135 140
- Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser 145 150 155 160
- Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
- Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile 180 185 190
- Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg 195 200 205
- Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly 210 215 220
- Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn 225 230 235 240
- Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
- Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe 260 265 270
- Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu 275 280 285
- Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln 290 295 300
- Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp 305 310 315 320
- Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly 325 330 335
- Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
- Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro 355 360 365
- Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro 370 375 380
- Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro 385 390 395 400
- Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

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Asn	Asp	Thr 435	Ser	Ile	Gln	Val	Ser 440	Trp	Leu	Ser	Leu	Phe 445	Thr	Val	Met
Ala	Tyr 450		Leu	Thr	Trp	Val 455	Lys	Met	Gly	His	Ser 460	Leu	Val	Gly	Gly
Ile 465		Gln	Glu	Arg	Ile 470	Val	Ser	Gly	Glu	Lys 475	Gln	His	Leu	Ser	Leu 480
Val	Asn	Leu	Glu	Pro 485	Arg	Ser	Thr	Tyr	Arg 490	Ile	Cys	Leu	Val	Pro 495	Leu
Asp	Ala	Phe	Asn 500	Tyr	Arg	Ala	Val	Glu 505	Asp	Thr	Ile	Cys	Ser 510	Glu	Ala
Thr	Thr	His 515	Ala	Ser	Tyr	Leu	Asn 520	Asn	Gly	Ser	Asn	Thr 525	Ala	Ser	Ser
His	Glu 530	Gln	Thr	Thr	Ser	His 535	Ser	Met	Gly	Ser	Pro 540	Phe	Leu	Leu	Ala
Gly 545	Leu	Ile	Gly	Gly	Ala 550	Val	Ile	Phe	Val	Leu 555	Val	Val	Leu	Leu	Ser 560
Val	Phe	Cys	Trp	His 565	Met	His	Lys	Lys	Gly 570	Arg	Tyr	Thr	Ser	Gln 575	Lys
Trp	Lys	Tyr	Asn 580	Arg	Gly	Arg	Arg	Lys 585	Asp	Asp	Tyr	Суѕ	Glu 590	Ala	Gly
Thr	Lys	Lys 595	Asp	Asn	Ser	Ile	Leu 600	Glu	Met	Thr	Glu	Thr 605	Ser	Phe	Gln
Ile	Val 610	Ser	Leu	Asn	Asn	Asp 615	Gln	Leu	Leu	Lys	Gly 620	Asp	Phe	Arg	Leu
Gln 625	Pro	Ile	Tyr	Thr	Pro 630	Asn	Gly	Gly	Ile	Asn 635	Tyr	Thr	Asp	Cys	His 640
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<400> 31 acgcagattt gagaaggctg tc	22
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<212> PRT

<213> Homo sapiens

<400> 34

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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu 35 40 45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser 50 55 60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile 65 70 75 80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val 85 90 95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys 100 105 110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg 115 120 125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu 130 135 140

Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn 145 150 155 160

Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser 165 170 175

Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe 180 185 190

Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205

Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln 210 215 220

Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

225					230					235					240
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Pro	Gly	Ser	Tyr 260	Val	Cys	Arg	Cys	Lys 265	Gln	Gly	Tyr	Ile	Leu 270	Asn	Ser
Asp	Gln	Thr 275	Thr	Cys	Arg	Ile	Gln 280	Asp	Leu	Cys	Ala	Met 285	Glu	Asp	His
Asn	Cys 290	Glu	Gln	Leu	Cys	Val 295	Asn	Val	Pro	Gly	Ser 300	Phe	Val	Cys	Gln
Cys 305	Tyr	Ser	Gly	Tyr	Ala 310	Leu	Ala	Glu	Asp	Gly 315	Lys	Arg	Cys	Val	Ala 320
Val	Asp	Tyr	Cys	Ala 325	Ser	Glu	Asn	His	Gly 330	Cys	Glu	His	Glu	Cys 335	Val
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Lys	Pro 370	Gly	Cys	Glu	His	Glu 375	Cys	Val	Asn	Met	Glu 380	Glu	Ser	Tyr	Tyr
Cys 385	Arg	Cys	His	Arg	Gly 390	Tyr	Thr	Leu	Asp	Pro 395	Asn	Gly	Lys	Thr	Cys 400
Ser	Arg	Val	Asp	His 405	Cys	Ala	Gln	Gln	Asp 410	His	Gly	Cys	Glu	Gln 415	Leu
Cys	Leu	Asn	Thr 420	Glu	Asp	Ser	Phe	Val 425	Cys	Gln	Cys	Ser	Glu 430	Gly	Phe
Leu	Ile	Asn 435	Glu	Asp	Leu	Lys	Thr 440	Cys	Ser	Arg	Val	Asp 445	Tyr	Cys	Leu
Leu	Ser 450	Asp	His	Gly	Cys	Glu 455	Tyr	Ser	Cys	Val	Asn 460	Met	Asp	Arg	Ser
Phe 465	Ala	Cys	Gln	Сув	Pro 470	Glu	Gly	His	Val	Leu 475	Arg	Ser	Asp	Gly	Lys 480
Thr	Cys	Ala	Lys	Leu 485	Asp	Ser	Cys	Ala	Leu 490	Gly	Asp	His	Gly	Cys 495	Glu
His	Ser	Cys	Val 500	Ser	Ser	Glu	Asp	Ser 505	Phe	Val	Cys	Gln	Cys 510	Phe	Glu

- Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val 515 520 525
- Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp 530 540
- Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp 545 550 555 560
- Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly 565 570 575
- Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys 580 585 590
- Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys 595 600 605
- Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser 610 620
- Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
- Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu 645 650 655
- Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn 660 665 670
- Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly 675 680 685
- Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser 690 695 700
- Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg 705 710 715 720
- Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
 725 730 735
- Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly 740 745 750
- Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
 755 760 765
- Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
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- Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser 785 790 795 800

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Gln	Pro	Thr	Glu 820	Ser	Glu	Pro	Val	Thr 825	Ile	Asn	Ile	Gln	Asp 830	Leu	Leu	
Ser	Cys	Ser 835	Asn	Phe	Ala	Val	Gln 840	His	Arg	Tyr	Leu	Phe 845	Glu	Glu	Asp	
Asn	Leu 850	Leu	Arg	Ser	Thr	Gln 855	Lys	Leu	Ser	His	Ser 860	Thr	Lys	Pro	Ser	
Gly 865	Ser	Pro	Leu	Glu	Glu 870	Lys	His	Asp	Gln	Cys 875	Lys	Cys	Glu	Asn	Leu 880	
Ile	Met	Phe	Gln	Asn 885	Leu	Ala	Asn	Glu	Glu 890	Val	Arg	Lys	Leu	Thr 895	Gln	
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Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
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Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
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Pro	Ser	Ile	Gly 420	Ile	Lys	Asp	Tyr	Asn 425		Leu	Thr	Arg	Ile 430	Thr	Glr
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Phe	Trp 450	Phe	Phe	Ser	Glu	Ile 455		Ser	Thr	Arg	Thr 460		Ile	His	Lys

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Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu 485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys 545 550 555 560

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Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu 610 615 620

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Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln 660 665 670

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- Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe 145 150 155 160
- Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
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- Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe 195 200 205
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- Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser 225 230 235 240
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- Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro 305 310 315 320
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Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala 100 105 110

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Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val 195 200 205

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- Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly 290 295 300

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Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala 435 440 445

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Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu 485 490 495

Cys Ile Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr 530 535 540

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- Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser 210 215 220
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oligonucleotide probe

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- Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly 65 70 75 80
- Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu 85 90 95
- Glu Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
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- Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu 115 120 125
- Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala 130 135 140
- Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met 145 150 155 160
- Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu 165 170 175
- Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr 180 185 190
- Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro 195 200 205
- Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val 210 215 220
- Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly 225 230 235 240
- Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys 245 250 255
- Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu 260 265 270
- Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr 275 280 285
- Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg 290 295 300
- Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro 305 310 315 320
- Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln 325 330 335
- Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

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Ile	e Phe	Val	Ser	Thr 405	Ala	Val	Val	Val	Leu 410	Val	Ile	Leu	Thr	Met 415	Thr	
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Pro	Ala 450	Ala	Leu	Gly	Ser	Ser 455		Ala	His	Cys	Thr 460	Asn	.Asn	Gly	Val	
Ly:	s Val	Gly	Asp	Cys	Asp 470	Leu	Arg	Asp	Arg	Ala 475	Glu	Gly	Ala	Leu	Leu 480	
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			-3-3			2										
	10> 9 11> 2															
	12> D 13> A		icia	l Se	quen	ce										
	20> 23> D	escr ligo						Seq	uenc	e: S	ynth	etic				
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Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
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Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
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55

- Val Pro Glu Gly Lys Val Val Leu Asn Phe Arg Phe Ile Asp Leu 65 70 75 80
- Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
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- His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro 100 105 110
- Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser 115 120 125
- Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala 130 135 140
- Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg 145 150 155 160
- Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro 165 170 175
- Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu 180 185 190
- Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
 195 200 205
- Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala 210 215 220
- Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val 225 230 235 240
- Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu 245 250 255
- Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu 260 265 270
- Pro Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr 275 280 285
- Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr 290 295 300
- Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly 305 310 315 320
- Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
- Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

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Leu Leu Arg 370	Arg Gly Leu	Asn Tyr 375	Ile Ile		Gly Gln 380	Val Gly	Glu
Asp Gly Arg 385	Gly Lys Ile 390	Met Pro	Asn Ser	Phe 3	Ile Met	Met Phe	Lys 400
Thr Lys Asn	Gln Lys Leu 405	Leu Asp	Ala Leu 410		Asn Lys	Gln Cys 415	
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<213> Homo sapiens

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Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr 35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile 50 55 60

- Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu 65 70 75 80
- Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly 85 90 95
- Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser 100 105 110
- Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro 115 120 125
- Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro 130 135 140
- Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu 145 150 155 160
- Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly 165 170 175
- Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Glu Ala Cys 180 185 190
- Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His 195 200 205
- Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro 210 215 220
- Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His 225 230 235 240
- Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys 245 250 255
- Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg 260 265 270
- Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg 275 280 285
- Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu 290 295 300
- Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln 305 310 315 320
- Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr 325 330 335
- Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala 340 345 350

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- Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln 65 70 75 80
- Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr 85 90. 95
- His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro As
n Ser Glu 100 105 110
- Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala 115 120 125
- Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg 130 135 140
- Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr 145 150 155 160
- Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys 165 170 175
- Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg 180 185 190
- Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu 195 200 205
- Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln 210 215 220
- Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu 225 230 235 240
- Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro 245 250 255
- Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu 260 265 270
- Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe 275 280 285
- Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu 290 295 300
- Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu 305 310 315 320
- Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr 325 330 335

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<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 115
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 116
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ataggagttg aagcagcgct gc
<210> 117
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<223> Description of Artificial Sequence: Synthetic
       oligonucleotide probe
<400> 117
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<210> 118
<211> 1857
<212> DNA
<213> Homo sapiens
<400> 118
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aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
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aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtggaag 240
tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagetca tegtgettgt geetecatee aageetacag ttaacateee etectetgee 480
accattggga accgggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
tacacctggt tcaaagatgg gatagtgatg cctacgaatc ccaaaagcac ccgtgccttc 600
agcaactett cetatgteet gaateecaca acaggagage tggtetttga teecetgtea 660
gcctctgata ctggagaata cagctgtgag gcacggaatg ggtatgggac acccatgact 720
tcaaatgctg tgcgcatgga agctgtggag cggaatgtgg gggtcatcgt ggcagccgtc 780
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teggatgtgt ttttaataat gteagetatg tgeeceatee teetteatge ceteecteec 1140
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tctagagcgg gaattagagg ctagagcggc tgaaatggtt gtttggtgat gacactgggg 1440
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cagaggetga ggeaggegga teacetgagg tegggagtte gggateagee tgaecaacat 1740
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<211> 299
<212> PRT
<213> Homo sapiens
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             20
Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
                                                  45
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Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe

90

55

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

<210> 121

<211> 50

<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
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<210> 122 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 122 acacctggtt caaagatggg	20
<210> 123 <211> 24 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 123 taggaagagt tgctgaaggc acgg	24
<210> 124 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe	
<400> 124 ttgccttact caggtgctac	20
<210> 125 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	

oligonucleotide probe

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<400> 125
                                                                  20
actcagcagt ggtaggaaag
<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens
<400> 126
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gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
geetggagge egeegegage eegettteea eecegacete tgeecaggee geaggeecea 180
getcaggetc gtgcccaccc accaagttcc agtgccgcac cagtggctta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagcc atgtacccag aaagggcaat gcccaccgcc ccctggcctc ccctgcccct 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggegetgega eggeeaceca gaetgteeeg acteeagega egagetegge tgtggaacea 540
atgagatect eceggaaggg gatgecaeaa ecatggggee eeetgtgaee etggagagtg 600
teacetetet caggaatgee acaaceatgg ggeeceetgt gaceetggag agtgteecet 660
ctgtcgggaa tgccacatcc tcctctgccg gagaccagtc tggaagccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctcctcttt 780
tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840
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agctaggatg gggaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140
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aagttgcttc
<210> 127
<211> 282
<212> PRT
<213> Homo sapiens
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Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
                              40
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
                          55
     50
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
                                          75
                      70
 65
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Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln 85 90 95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly 100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Leu Arg Asn Cys Ser 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 145 150 155

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

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<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 129
                                                                   24
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<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 130
                                                                   50
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc
<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (1837)
<223> a, t, c or g
<400> 131
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gggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagaccca 120
cagactettg caagetggat geeetetgtg gatgaaagat gtateatgga atgaaceega 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactettggc egtgateetg tggttteage tggegetgtg etteggeeet geacagetea 300
cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatggcttca 360
ggacccccag cggaggggtt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
ategetgett teeeggattt aaacttgatg ggtetgegta tettgagtge ttacaaaace 840
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agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcgttca 1140
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cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
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cqqcaqagga ggtggcatcc accagcccag gcatccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
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<210> 132
<211> 490
<212> PRT
<213> Homo sapiens
<400> 132
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Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
                                 25
             20
Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
                                              60
                         55
Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
                                          75
 65
Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
                                      90
Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
                                 105
            100
Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
                             120
        115
Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
                                             140
                         135
Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
145
                     150
                                         155
Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
                                     170
                 165
Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn
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			180					185					190		
Ile	Ser	Glu 195	Leu	Gln	Thr	Ser	Phe 200	Pro	Val	Gly	Thr	Val 205	Ile	Ser	Tyr
Arg	Cys 210	Phe	Pro	Gly	Phe	Lys 215	Leu	Asp	Gly	Ser	Ala 220	Tyr	Leu	Glu	Cys
Leu 225	Gln	Asn	Leu	Ile	Trp 230	Ser	Ser	Ser	Pro	Pro 235	Arg	Cys	Leu	Ala	Leu 240
Glu	Ala	Gln	Val	Cys 245	Pro	Leu	Pro	Pro	Met 250	Val	Ser	His	Gly	Asp 255	Phe
Val	Cys	His	Pro 260	Arg	Pro	Cys	Glu	Arg 265	Tyr	Asn	His	Gly	Thr 270	Val	Val
Glu	Phe	Tyr 275	Cys	Asp	Pro	Gly	Tyr 280	Ser	Leu	Thr	Ser	Asp 285	Tyr	Lys	Tyr
Ile	Thr 290	Cys	Gln	Tyr	Gly	Glu 295	Trp	Phe	Pro	Ser	Tyr 300	Gln	Val	Tyr	Cys
Ile 305	Lys	Ser	Glu	Gln	Thr 310	Trp	Pro	Ser	Thr	His 3 1 5	Glu	Thr	Leu	Leu	Thr 320
Thr	Trp	Lys	Ile	Val 325	Ala	Phe	Thr	Ala	Thr 330		Val	Leu	Leu	Val 335	Leu
Leu	Leu	Val	Ile 340	Leu	Ala	Arg	Met	Phe 345		Thr	Lys	Phe	Lys 350	Ala	His
Phe	Pro	Pro 355		Gly	Pro	Pro	Arg 360		Ser	Ser	Ser	Asp 365	Pro	Asp	Phe
Val	Val 370	Val	Asp	Gly	· Val	Pro 375		Met	Leu	. Pro	Ser 380		Asp	Glu	Ala
Val 385	Ser	Gly	Gly	Leu	Ser 390		Leu	Gly	Pro	Gly 395	Tyr	Met	Ala	Ser	Val 400
Gly	Gln	Gly	Cys	Pro 405		. Pro	Val	Asp	410		Ser	Pro	Pro	Ala 415	
Pro	Gly	Ser	Gly 420		Thr	. Asp	Thr	Gly 425		Gly	Glu	Ser	Glu 430		Cys
Asp	Ser	Val 435		Gly	ser Ser	Ser	Glu 440		ı Lev	ı Glr	. Ser	Leu 445	Tyr	Ser	Pro
Pro	Arg		: Gln	Glu	. Ser	Thr 455		Pro	Ala	a Ser	Asp 460		n Pro	Asp	ıl.

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465
                    470
His Ala His Trp Val Leu Phe Leu Arg Asn
                                     490
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<210> 133
<211> 23
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 133
                                                                    23
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<210> 134
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 134
                                                                    23
agccaggatc gcagtaaaac tcc
<210> 135
<211> 50
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens
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ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgcctgc 240
tgagtgcctc ggatttggac ctcagaggag ggcagccagt ctgccgggga gggacacaga 300
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ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gegaggtetg egtggteatg taccateage categgeace egetggeate ggaggeecet 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
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gagaagetge ettgaatetg geetacatee taateeceag eatteecett eteeteetee 900
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atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
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agcaggaaaa aaaaa
<210> 137
<211> 382
<212> PRT
<213> Homo sapiens
<400> 137
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Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
                                  25
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
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Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn 85 90 95

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser

70

75

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Glu
100 105 110

- Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr 115 120 125
- Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser 130 135 140
- Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro 145 150 155 160
- Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys 165 170 175
- Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala 180 185 190
- Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro 195 200 205
- Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys 210 215 220
- Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser 225 230 235 240
- Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val 245 250 255
- Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys 260 265 270
- Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp 275 280 285
- Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala 290 295 300
- Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly 305 310 315 320
- Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val 325 330 335
- Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly 340 345 350
- Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg 355 360 365
- Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr 370 375 380

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<211> 50
<212> DNA
<213> Artificial Sequence
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Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
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Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly 225 230 235 235

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Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile 275 280 285

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Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp 340 345 350

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110

85

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Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro 130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr 145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys 165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn 180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly 210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp 225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg 245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn 260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly 275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly 290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln 305 310 315 320

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Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
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Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr 180 185 190

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Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

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Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
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Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp 115 120 125

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Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile 195 200 205

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2477

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- Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
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- Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly 210 215 220
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- His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
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- Ile Asn Leu Gl
n Ile Lys Glu Arg Leu Gl
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n Gly Glu $420 \hspace{1.5cm} 425 \hspace{1.5cm} 430 \hspace{1.5cm}$
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Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln 595 600 605

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20

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- Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Trp Trp Gln Lys
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- Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
- Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe 100 105 110
- Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr 115 120 125
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- Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp 145 150 155 160
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- Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys 195 200 205
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- Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser 225 230 235 240
- Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr 245 250 255
- Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly 260 265 270
- Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro 275 280 285
- His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr 290 295 300
- Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val 305 310 315 320
- Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn 325 330 335

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         35
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Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
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                                         75
Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
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Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
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Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
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Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser 165 170 175

Thr Ile Pro Ala Pro Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser 180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu 195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala 210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu 225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe 245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn 260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala 275 280 285

Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro 290 295 300

Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala 305 310 315 320

Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

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<400> 202

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<210> 203

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<212> DNA
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Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
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Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
130 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val 145 150 155 160

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Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg 225 230 235 240

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<220>

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Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala

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Tyr 225	Ile	Ala	Asp	Leu	Tyr 230	Ser	Ala	Glu	Pro	Gly 235	Glu	Glu	Glu	Pro	Ala 240
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Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys 145 150 155

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Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala 180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln 195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser 210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly 225 230 235 240

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- Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val 275 280 285
- Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro 290 295 300
- Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys 315 310 315
- Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp 325 330 335
- Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr 340 345 350
- His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile 355 360 365
- Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg 370 375 380
- Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser 385 390 395 400
- Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg 405 410 415
- Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala 420 425 430
- Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp 435 440 445
- Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser 450 455 460
- Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp 465 470 475 480
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- Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
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- Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
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- Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser 130 135 140
- His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln 145 150 155 160
- Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
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- Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
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- Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys 195 200 205
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- Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240
- Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255
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- Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe 275 280 285
- Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val 290 295 300
- Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu 305 310 315 320
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Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu 50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu 65 70 75

Leu Gln Ser Asn Ser Ile Val Arg Val Asp Gln Ser Glu Leu Gly
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Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu 110 115 120

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Gly Gln Gly Leu	Glu Leu Arg 530	Val Gln Glu 5	Thr His Pro	Tyr His 540
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Phe Ala Asp Ala	His Thr Gln 605	Leu Ala Cys 1	Val Trp Ala	Arg Thr 615
Lys Glu Ala Thr	Ser Cys His 620	Arg Ala Leu 6 625	Gly Asp Arg	Pro Gly 630
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Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
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Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys

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T7 - 3	~ 1	**- 7	TT!	290	6 1	.	.	a	295			~ 1	~ 1	300
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 ccaggetgcc agtetectat ttgtggataa tecegtgggc actgggttca 400
 gttatgtgaa tggtagtggt gcctatgcca aggacctggc tatggtggct 450
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aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750 qccqtaaata aqqqqctcta cagagaggcc acagagctgt gggggaaagc 800 agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900 cagagecace tagtttgtet ttgteagege caegtgagae acetaeaaeg 950 agatgcctta agccagctca tgaatggccc catcagaaag aagctcaaaa 1000 ttattcctqa qqatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050 aacatggagg aggacttcat gaagccagtc attagcattg tggacgagtt 1100 gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150 tcgtagatac catgggtcag gaggcctggg tgcggaaact gaagtggcca 1200 gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250 taaatetttg gaaacatetg ettttgteaa gteetacaag aacettgett 1300 tctactqqat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350 atggctctga agatgatgag actggtgact cagcaagaat aggatggatg 1400 gggctggaga tgagctggtt tggccttggg gcacagagct gagctgaggc 1450 cgctgaagct gtaggaagcg ccattcttcc ctgtatctaa ctggggctgt 1500 gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550 ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600 taaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu
1 5 10 15

Leu Leu Pro Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
35 40 45

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln 65 Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe 145 150 140 Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly 190 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys 215 220 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys 245 250 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr 260 265 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser 275 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly

	305	310	3:	15
Pro Ile Arg Lys	Lys Leu Lys 320	Ile Ile Pro Glu 325		rp 30
Gly Gly Gln Ala	Thr Asn Val	Phe Val Asn Met 340		he 45
Met Lys Pro Val	Ile Ser Ile 350	Val Asp Glu Leu 355		ly 60
Ile Asn Val Thr	Val Tyr Asn 365	Gly Gln Leu Asp 370		sp 75
Thr Met Gly Gln	Glu Ala Trp 380	Val Arg Lys Leu 385		lu 90
Leu Pro Lys Phe	Ser Gln Leu 395	Lys Trp Lys Ala 400		.sp 05
Pro Lys Ser Leu	Glu Thr Ser 410	Ala Phe Val Lys 415		sn 20
Leu Ala Phe Tyr	Trp Ile Leu 425	Lys Ala Gly His 430		er 35
Asp Gln Gly Asp	Met Ala Leu 440	Lys Met Met Arg 445		1n 50
Gln Glu				

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg 1 5 10 15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20 25 30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75

Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu 80 85 90

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

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Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
                110
Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
                125
                                                         135
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
                                                         165
                155
Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
                185
                                     190
Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
                200
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
                215
Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
                                     235
                                                         240
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
                                     250
Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
                                     265
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
                275
                                                         285
Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
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Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
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<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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tgatggctac tgggtggtca gcaacagagt gcccattcca tgggtgtccg 1450 gaacctegge etetaeteea gtgtttgggg ggateetate ettgateaat 1500 gagcacagga tccttagtgg ccgccccct cttggctttc tcaacccaag 1550 gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600 atgagteetg tetggatgaa gaggtagagg geeagggttt etgetetggt 1650 cctggctggg atcctgtaac aggctgggga acaccaactt cccagctttg 1700 ctgaagactc tactcaaccc ctgacccttt cctatcagga gagatggctt 1750 gtcccctgcc ctgaagctgg cagttcagtc ccttattctg ccctgttgga 1800 agecetgetg aaccetcaac tattgaetge tgeagacage ttateteect 1850 aaccetqaaa tgetgtgage ttgacttgae teecaaecet accatgetee 1900 atcatactca gqtctcccta ctcctgcctt agattcctca ataagatgct 1950 gtaactagca ttttttgaat gcctctccct ccgcatctca tctttctctt 2000 ttcaatcaqq cttttccaaa qqqttqtata caqactctqt qcactatttc 2050 acttgatatt cattccccaa ttcactgcaa ggagacctct actgtcaccg 2100 tttactcttt cctaccctqa catccaqaaa caatqqcctc caqtqcatac 2150 tteteaatet tigetitatg geetiteeat eatagitgee eacteeetet 2200 ccttacttag cttccaggtc ttaacttctc tgactactct tgtcttcctc 2250 tctcatcaat ttctgcttct tcatggaatg ctgaccttca ttgctccatt 2300 tgtagatttt tgctcttctc agtttactca ttgtcccctg gaacaaatca 2350 ctgacatcta caaccattac catctcacta aataagactt tctatccaat 2400 aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

Met Gly Leu Gln Ala Cys Leu Leu Gly Leu Phe Ala Leu Ile Leu 1 5 10 15

Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr

				20					25					30
Leu	Pro	Pro	Gly	Trp 35	Val	Ser	Leu	Gly	Arg 40	Ala	Asp	Pro	Glu	Glu 45
Glu	Leu	Ser	Leu	Thr 50	Phe	Ala	Leu	Arg	Gln 55	Gln	Asn	Val	Glu	Arg 60
Leu	Ser	Glu	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr	Gly	Lys	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro	Ser	Pro	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala	Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala	Glu	Phe	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165
His	Val	Asp	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu	His	Leu	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu	Thr	Ser	Gln	Asp 215	Val	Gly	Ser	Gly	Thr 220	Ser	Asn	Asn	Ser	Gln 225
Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser	Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile	Glu	Ala	Ser	Leu 275	Asp	Val	Gln	Tyr	Leu 280		Ser	Ala	Gly	Ala 285

Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly 290 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser 305 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp 320 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met Lys Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp 355 360 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly 385 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp 395 Tyr Ile Ser Gly Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser 415 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Pro His 430 435 Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg 460 Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val 480 470 475 Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser 490 Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln 505 510 500 His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser 520 515 Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu 545 550 555 Cys

<210> 260 <211> 1638 <212> DNA <213> Homo Sapien

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<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

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1	5	10	15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro 20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr 35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
50 55 60

Val Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu 65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu 80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

95 100 105

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser

Ser	Gly	Lys	Ser	Arg 125	Arg	Lys	Arg	Gln	Ile 130	Tyr	Gly	Tyr	Asp	Ser 135
Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	'Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Суз	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240
Ile	Gly	Met	Asp	Tyr 245	Asp	Tyr	Ala	Leu	Leu 250	Glu	Leu	Lys	Lys	Pro 255
His	Lys	Arg	Lys	Phe 260	Met	Lys	Ile	Gly	Val 265	Ser	Pro	Pro	Ala	Lys 270
Gln	Leu	Pro	Gly	Gly 275		Ile	His	Phe	Ser 280	Gly	Tyr	Asp	Asn	Asp 285
Arg	Pro	Gly	Asn	Leu 290	Val	Tyr	Arg	Phe	Cys 295	Asp	Val	Lys	Asp	Glu 300
Thr	Tyr	Asp	Leu	Leu 305		Gln	Gln	Cys	Asp 310		Gln	Pro	Gly	Ala 315
Ser	Gly	Ser	Gly	Val 320		Val	Arg	Met	Trp 325		Arg	Gln	. Gln	Gln 330
Lys	Trp	Glu	. Arg	Lys 335		Ile	Gly	Ile	Phe 340		Gly	His	Gln	Trp 345
Val	Asp	Met	Asn	Gly 350		Pro	Gln	Asp	Phe 355		. Val	. Ala	. Val	Arg 360
Ile	Thr	Pro	Leu	Lys 365		Ala	Gln	Ile	Cys 370		Trp	ıle	. Lys	Gly 375
Asn	Tyr	Leu	ı Asp	Cys 380		Glu	Gly							

<210> 262 <211> 1378 <212> DNA

<213> Homo Sapien

<400> 262 gcatcgccct gggtctctcg agcctgctgc ctgctccccc gccccaccag 50 ccatggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100 accttcacct ccctgctgct gctggcgtcg acagccatcc tcaatgcggc 150 caggatacet gttcccccag cetgtgggaa geeccagcag etgaaceggg 200 ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250 atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300 ctgggtgatc actgctgccc actgtttcaa ggacaacctg aacaaaccat 350 acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400 cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450 ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500 ccatacagtt ctcagagcgg gtcctgccca tctgcctacc tgatgcctct 550 atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650 ttectateat egacteggaa gtetgeagee atetgtaetg geggggagea 700 ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850 geogagegea acaggeoegg ggtetacate ageotetetg egeacegete 900 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950 ggggtgggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000 tectagggeg cagegggaeg egggetegg atetgaaagg eggeeagate 1050 cacatetgga tetggatetg eggeggeete gggeggttte eecegeegta 1100 aataggetea tetaceteta eetetggggg eeeggaegge tgetgeggaa 1150 aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200 catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250 cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgatttt 1300 ataaggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350 ataaattatt tattctccaa aaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

Met 1	Val	Val	Ser	Gly 5	Ala	Pro	Pro	Ala	Leu 10	Gly	Gly	Gly	Cys	Leu 15
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Asn	Ala	Ala	Arg	Ile 35	Pro	Val	Pro	Pro	Ala 40	Cys	Gly	Lys	Pro	Gln 45
Gln	Leu	Asn	Arg	Val 50	Val	Gly	Gly	Glu	Asp 55	Ser	Thr	Asp	Ser	Glu 60
Trp	Pro	Trp	Ile	Val 65	Ser	Ile	Gln	Lys	Asn 70	Gly	Thr	His	His	Cys 75
Ala	Gly	Ser	Leu	Leu 80	Thr	Ser	Arg	Trp	Val 85	Ile	Thr	Ala	Ala	His 90
Cys	Phe	Lys	Asp	Asn 95	Leu	Asn	Lys	Pro	Tyr 100	Leu	Phe	Ser	Val	Leu 105
Leu	Gly	Ala	Trp	Gln 110	Leu	Gly	Asn	Pro	Gly 115	Ser	Arg	Ser	Gln	Lys 120
Val	Gly	Val	Ala	Trp 125	Val	Glu	Pro	His	Pro 130	Val	Tyr	Ser	Trp	Lys 135
Glu	Gly	Ala	Cys	Ala 140	Asp	Ile	Ala	Leu	Val 145	Arg	Leu	Glu	Arg	Ser 150
Ile	Gln	Phe	Ser	Glu 155	Arg	Val	Leu	Pro	Ile 160	Cys	Leu	Pro	Asp	Ala 165
Ser	Ile	His	Leu	Pro 170	Pro	Asn	Thr	His	Cys 175	Trp	Ile	Ser	Gly	Trp 180

255

<210> 266 <211> 24

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Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
                                     190
                 185
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
                 200
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
                 215
                                     220
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
                                     250
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
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                                     265
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
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Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
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<212> PRT

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Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val
65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Gly Glu Asn Leu Phe 80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu 95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys
110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala 125 130 135

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Gln	Gly	Val	Glu	Glu 155	Thr	Asn	Ile	Glu	Leu 160	Leu	Val	Cys	Asn	Tyr 165
Glu	Pro	Pro	Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr	Pro	Cys	Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Cys	Lys	Asn	Ser 195
Leu	Cys	Glu	Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr	Leu	Val	Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp	Ser	Arg	Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
Pro	Ala	Phe	Leu	Val 245	Thr	Glu	Val	Ser	Gly 250	Ser	Leu	Ala	Thr	Lys 255
Ala	Leu	Pro	Ala	Val 260	Glu	Thr	Gln	Ala	Pro 265	Thr	Ser	Leu	Ala	Thr 270
Lys	Asp	Pro	Pro	Ser 275	Met	Ala	Thr	Glu	Ala 280	Pro	Pro	Cys	Val	Thr 285
Thr	Glu	Val	Pro	Ser 290	Ile	Leu	Ala	Ala	His 295	Ser	Leu	Pro	Ser	Leu 300
Asp	Glu	Glu	Pro	Val 305	Thr	Phe	Pro	Lys	Ser 310	Thr	His	Val	Pro	Ile 315
Pro	Lys	Ser	Ala	Asp 320	Lys	Val	Thr	Asp	Lys 325	Thr	Lys	Val	Pro	Ser 330
Arg	Ser	Pro	Glu	Asn 335		Leu	. Asp	Pro	Lys 340	Met	Ser	Leu	Thr	Gly 345
Ala	Arg	Glu	Leu	Leu 350		His	Ala	Gln	Glu 355		Ala	Glu	Ala	Glu 360
Ala	Glu	Leu	Pro	Pro 365		Ser	Glu	. Val	Leu 370		Ser	Val	Phe	Pro 375
Ala	Gln	Asp	Lys	Pro 380		Glu	. Leu	. Gln	. Ala 385		Leu	Asp	His	Thr 390
Gly	His	Thr	Ser	Ser		s Ser	Leu	Pro	Asn 400		Pro	Asn	Thr	Ser 405

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<211> 1059

<212> PRT

<213> Homo Sapien

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Ile	Leu	Pro	Glu	His 80	Leu	Lys	Glu	Phe	Gln 85	Ser	Leu	Glu	Thr	Leu 90
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Ala	Leu	Gln	Leu	Lys 110	Tyr	Leu	Tyr	Leu	Asn 115	Ser	Asn	Arg	Val	Thr 120
Ser	Met	Glu	Pro	Gly 125	Tyr	Phe	Asp	Asn	Leu 130	Ala	Asn	Thr	Leu	Leu 135
Val	Leu	Lys	Leu	Asn 140	Arg	Asn	Arg	Ile	Ser 145	Ala	Ile	Pro	Pro	Lys 150
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Arg	Ile	Ser	Pro	Asp 245	Ala	Trp	Glu	Phe	Cys 250	Gln	Lys	Leu	Ser	Glu 255
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Phe	Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	Asp 610	Ile	Gly	Val	Tyr	Ser 615
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Gly	Gly	Ser	Pro	Pro 665	Pro	Lys	Leu	Asn	Trp 670	Thr	Lys	Asp	Asp	Ser 675
Pro	Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690
Leu	Leu	Ile	Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705
Thr	Cys	Glu	Met	Ser 710	Asn	Thr	Leu	Gly	Thr 715	Glu	Arg	Gly	Asn	Val 720
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				740		Asp			745					750
Val	Ile	Ile	Ala	Val 755		Cys	Cys	Val	Val 760	Gly	Thr	Ser	Leu	Val 765
Trp	Val	Val	Ile	Ile 770		His	Thr	Arg	775		Asn	Glu	Asp	Cys 780
Ser	Ile	Thr	Asn	Thr 785		Glu	Thr	Asn	Leu 790		Ala	Asp	Ile	Pro 795
Ser	Tyr	Leu	Ser	Ser		Gly	Thr	Leu	. Ala		Arg	Gln	. Asp	Gly 810

Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr 830 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr 860 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His 880 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr 895 890 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp 930 925 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn 935 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu 960 955 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn 970 965 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu 985 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg 1005 995 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly 1015 1010 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn 1030 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro 1045 Asn Phe Gln Ser Tyr Asp Leu Asp Thr

<210> 291 <211> 2906 1055

<212> DNA <213> Homo Sapien

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tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300 ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400 ccaacttgag gtatttgaac cttgccatgt gcaaccttcg ggaaatccct 1450 aacctcacac cgctcataaa actagatgag ctggatcttt ctgggaatca 1500 tttatctgcc atcaggcctg gctctttcca gggtttgatg caccttcaaa 1550 aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgccttt 1600 gacaaccttc agtcactagt ggagatcaac ctggcacaca ataatctaac 1650 attactgcct catgacctct tcactccctt gcatcatcta gagcggatac 1700 atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750 tggtggataa aagacatggc cccctcgaac acagcttgtt gtgcccggtg 1800 taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850 attacttcac atgctatgct ccggtgattg tggagccccc tgcagacctc 1900 aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950 cctgacatct gtatcttgga ttactccaaa tggaacagtc atgacacatg 2000 gggcgtacaa agtgcggata gctgtgctca gtgatggtac gttaaatttc 2050 acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100 ttccgttggg aatactactg cttcagccac cctgaatgtt actgcagcaa 2150 ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200 ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250 agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300 gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350 agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550 catggaaagc cacctgccca tgcctgctat cgagcatgag cacctaaatc 2600 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650 ataaattcaa tacacagttc agtgcatgaa ccgttattga tccgaatgaa 2700 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800 tgactggct aaatctactg tttcaaaaaa gtgtctttac aaaaaacaa 2850 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900 caaaaa 2906

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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln 35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser 65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile 80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu 95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe 110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg 125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser

				155					160					165
Tyr	Ala	Phe	Asn	Arg 170	Ile	Pro	Ser	Leu	Arg 175	Arg	Leu	Asp	Leu	Gly 180
Glu	Leu	Lys	Arg	Leu 185	Ser	Tyr	Ile	Ser	Glu 190	Gly	Ala	Phe	Glu	Gly 195
Leu	Ser	Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu	Ile	Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu	Ser	Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly	Leu	Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln	Val	Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu	Ile	Asn	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu	Phe	Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn	Pro	Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
Ile	Lys	Asp	Met	Ala 320	Pro	Ser	Asn	Thr	Ala 325		Cys	Ala	Arg	Cys
Asn	Thr	Pro	Pro	Asn 335	Leu	Lys	Gly	Arg	Tyr 340		Gly	Glu	Leu	Asp 345
Gln	Asn	Tyr	Phe	Thr 350		Tyr	Ala	Pro	Val 355		Val	Glu	Pro	Pro 360
Ala	Asp	Leu	Asn	Val 365		Glu	Gly	Met	Ala 370		Glu	. Leu	. Lys	Сув 375
Arg	Ala	Ser	Thr	Ser 380		Thr	Ser	Val	Ser 385		Ile	Thr	Pro	Asn 390
Gly	Thr	Val	. Met	Thr 395		Gly	Ala	Tyr	Lys 400		. Arg	, Il∈	Ala	Val 405
Leu	Ser	Asp	Gly	Thr		. Asn	Phe	Thr	Asr.		Thr	· Val	Gln	Asp 420

Thr	Gly	Met	Tyr	Thr 425	Cys	Met	Val	Ser	Asn 430	Ser	Val	Gly	Asn	Thr 435
Thr	Ala	Ser	Ala	Thr 440	Leu	Asn	Val	Thr	Ala 445	Ala	Thr	Thr	Thr	Pro 450
Phe	Ser	Tyr	Phe	Ser 455	Thr	Val	Thr	Val	Glu 460	Thr	Met	Glu	Pro	Ser 465
Gln	Asp	Glu	Ala	Arg 470	Thr	Thr	Asp	Asn	Asn 475	Val	Gly	Pro	Thr	Pro 480
Val	Val	Asp	Trp	Glu 485	Thr	Thr	Asn	Val	Thr 490	Thr	Ser	Leu	Thr	Pro 495
Gln	Ser	Thr	Arg	Ser 500	Thr	Glu	Lys	Thr	Phe 505	Thr	Ile	Pro	Val	Thr 510
Asp	Ile	Asn	Ser	Gly 515	Ile	Pro	Gly	Ile	Asp 520	Glu	Val	Met	Lys	Thr 525
Thr	Lys	Ile	Ile	Ile 530	Gly	Cys	Phe	Val	Ala 535	Ile	Thr	Leu	Met	Ala 540
Ala	Val	Met	Leu	Val 545	Ile	Phe	Tyr	Lys	Met 550	Arg	Lys	Gln	His	His 555
Arg	Gln	Asn	His	His 560		Pro	Thr	Arg	Thr 565	Val	Glu	Ile	Ile	Asn 570
Val	Asp	Asp	Glu	Ile 575		Gly	Asp	Thr	Pro 580	Met	Glu	Ser	His	Leu 585
Pro	Met	Pro	Ala	Ile 590		His	Glu	His	Leu 595		His	Tyr	Asn	Ser 600
Tyr	Lys	Ser	Pro	Phe 605		His	Thr	Thr	Thr 610	Val	Asn	Thr	Ile	Asn 615
Ser	: Ile	His	Ser	Ser 620		. His	Glu	. Pro	625	Leu	lle	Arg	Met	Asn 630
Ser	Lys	s Asp) Asn	Val 635		ı Glu	ı Thr	Gln	11∈ 640					

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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gtttccctcc tgctgtttgg gggcatgaaa gggcttcgcc gccgggagta 100 aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150 gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200 gegeeggetg ggagettegg gtagagaeet aggeegetgg accgegatga 250 gegegeegag ceteegtgeg egegeegegg ggttgggget getgetgtge 300 geggtgetgg ggegegetgg ceggteegae ageggeggte geggggaaet 350 egggeagece tetggggtag eegeegageg eccatgeece actaeetgee 400 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450 cccgagccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500 attatettte ateaaggeaa gtteeatgag ceacetteaa ageettegag 550 aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600 gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650 aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700 ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750 ctcaaatatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800 gtattttgac aatttggcca acacactcct tgtgttaaag ctgaacagga 850 accgaatete agetateeea eecaagatgt ttaaaetgee eeaaetgeaa 900 catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950 ccaaggcctt ggtgctctga agtctctgaa aatgcaaaga aatggagtaa 1000 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050 cagetggace ataacaacet aacagagatt accaaagget ggetttacgg 1100 cttgctgatg ctgcaggaac ttcatctcag ccaaaatgcc atcaacagga 1150 tcagccctga tgcctgggag ttctgccaga agctcagtga gctggaccta 1200 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250 cttactaaat acactgcaca ttgggaacaa cagagtcagc tacattgctg 1300 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350 aatgaaattt cctggactat tgaagacatg aatggtgctt tctctgggct 1400 tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450 ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500 gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550 actgcaacaa ttgcatttaa atacatcaag cettttgtge gattgeeage 1600 taaaatggct cccacagtgg gtggcggaaa acaactttca gagctttgta 1650 aatgccagtt gtgcccatcc tcagctgcta aaaggaagaa gcatttttgc 1700 tgttagccca gatggctttg tgtgtgatga ttttcccaaa ccccagatca 1750 cggttcagcc agaaacacag tcggcaataa aaggttccaa tttgagtttc 1800 atctgctcag ctgccagcag cagtgattcc ccaatgactt ttgcttggaa 1850 aaaagacaat gaactactgc atgatgctga aatggaaaat tatgcacacc 1900 teegggeeca aggtggegag gtgatggagt ataccaccat cetteggetg 1950 cgcgaggtgg aatttgccag tgaggggaaa tatcagtgtg tcatctccaa 2000 tcactttggt tcatcctact ctgtcaaagc caagcttaca gtaaatatgc 2050 ttccctcatt caccaagacc cccatggatc tcaccatccg agctggggcc 2100 atggcacgct tggagtgtgc tgctgtgggg cacccagccc cccagatagc 2150 ctggcagaag gatgggggca cagacttccc agctgcacgg gagagacgca 2200 tgcatgtgat gcccgaggat gacgtgttct ttatcgtgga tgtgaagata 2250 gaggacattg gggtatacag ctgcacagct cagaacagtg caggaagtat 2300 ttcagcaaat gcaactctga ctgtcctaga aacaccatca tttttgcggc 2350 cactgttgga ccgaactgta accaagggag aaacagccgt cctacagtgc 2400 attgctggag gaagccctcc ccctaaactg aactggacca aagatgatag 2450 cccattggtg gtaaccgaga ggcacttttt tgcagcaggc aatcagcttc 2500 tgattattgt ggactcagat gtcagtgatg ctgggaaata cacatgtgag 2550 atgtctaaca cccttggcac tgagagagga aacgtgcgcc tcagtgtgat 2600 ccccactcca acctgcgact cccctcagat gacagcccca tcgttagacg 2650 atgacggatg ggccactgtg ggtgtcgtga tcatagccgt ggtttgctgt 2700 gtggtggca cgtcactcgt gtgggtggtc atcatatacc acacaaggcg 2750 gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800 cagatattcc tagttatttg tcatctcagg gaacgttagc tgacaggcag 2850 gatgggtacg tgtcttcaga aagtggaagc caccaccagt ttgtcacatc 2900 ttcaggtgct ggatttttct taccacaaca tgacagtagt gggacctgcc 2950 atattgacaa tagcagtgaa gctgatgtgg aagctgccac agatctgttc 3000 ctttgtccgt ttttgggatc cacaggccct atgtatttga agggaaatgt 3050 gtatggctca gatccttttg aaacatatca tacaggttgc agtcctgacc 3100 caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150 gagtgctacc catgttctca tccttcagaa gaatcctgcg aacggagctt 3200 cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250 actctcacaa tgaaggacct ggaatgaaaa atctgtgtct aaacaagtcc 3300 tctttagatt ttagtgcaaa tccagagcca gcgtcggttg cctcgagtaa 3350 ttctttcatg ggtacctttg gaaaagctct caggagacct cacctagatg 3400 cctattcaag ctttggacag ccatcagatt gtcagccaag agccttttat 3450 ttgaaagctc attcttcccc agacttggac tctgggtcag aggaagatgg 3500 gaaagaaagg acagattttc aggaagaaaa tcacatttgt acctttaaac 3550 agactttaga aaactacagg actccaaatt ttcagtctta tgacttggac 3600 acatagactg aatgagacca aaggaaaagc ttaacatact acctcaagtg 3650 aacttttatt taaaagagag agaatcttat gttttttaaa tggagttatg 3700 aattttaaaa ggataaaaat gctttattta tacagatgaa ccaaaattac 3750 aaaaagttat gaaaattttt atactgggaa tgatgctcat ataagaatac 3800 ctttttaaac tatttttaa ctttgtttta tgcaaaaaag tatcttacgt 3850 aaattaatga tataaatcat gattatttta tgtatttta taatgccaga 3900 tttcttttta tggaaaatga gttactaaag cattttaaat aatacctgcc 3950 ttgtaccatt ttttaaatag aagttacttc attatatttt gcacattata 4000 aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp 65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys 80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu 95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser 110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu 125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu 140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro 155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr 170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu 185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys 200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

		215					220					225
Lys Ile Ly		Val 230	Asp	Gly	Leu	Thr	Phe 235	Gln	Gly	Leu	Gly	Ala 240
Leu Lys Se		Lys 245	Met	Gln	Arg	Asn	Gly 250	Val	Thr	Lys	Leu	Met 255
Asp Gly Ala		Trp 260	Gly	Leu	Ser	Asn	Met 265	Glu	Ile	Leu	Gln	Leu 270
Asp His As:		Leu 275	Thr	Glu	Ile	Thr	Lys 280	Gly	Trp	Leu	Tyr	Gly 285
Leu Leu Me		Gln 290	Glu	Leu	His	Leu	Ser 295	Gln	Asn	Ala	Ile	Asn 300
Arg Ile Se	r Pro	Asp 305	Ala	Trp	Glu	Phe	Cys 310	Gln	Lys	Leu	Ser	Glu 315
Leu Asp Le	ı Thr	Phe 320	Asn	His	Leu	Ser	Arg 325	Leu	Asp	Asp	Ser	Ser 330
Phe Leu Gl	y Leu	Ser 335	Leu	Leu	Asn	Thr	Leu 340	His	Ile	Gly	Asn	Asn 345
Arg Val Se	r Tyr	Ile 350	Ala	Asp	Cys	Ala	Phe 355	Arg	Gly	Leu	Ser	Ser 360
Leu Lys Th	r Leu	Asp 365	Leu	Lys	Asn	Asn	Glu 370	Ile	Ser	Trp	Thr	Ile 375
Glu Asp Me	t Asn	Gly 380	Ala	Phe	Ser	Gly	Leu 385	Asp	Lys	Leu	Arg	Arg 390
Leu Ile Le	u Gln	Gly 395	Asn	Arg	Ile	Arg	Ser 400	Ile	Thr	Lys	Lys	Ala 405
Phe Thr Gl	y Leu	Asp 410	Ala	Leu	Glu	His	Leu 415	Asp	Leu	Ser	Asp	Asn 420
Ala Ile Me	t Ser	Leu 425	Gln	Gly	Asn	Ala	Phe 430	Ser	Gln	Met	Lys	Lys 435
Leu Gln Gl	n Leu	His 440	Leu	Asn	Thr	Ser	Ser 445	Leu	Leu	Cys	Asp	Cys 450
Gln Leu Ly	s Trp	Leu 455	Pro	Gln	Trp	Val	Ala 460	Glu	Asn	Asn	Phe	Gln 465
Ser Phe Va	l Asn	Ala 470	Ser	Cys	Ala	His	Pro 475	Gln	Leu	Leu	Lys	Gly 480

Arg	Ser	Ile	Phe	Ala 485	Val	Ser	Pro	Asp	Gly 490	Phe	Val	Cys	Asp	Asp 495
Phe	Pro	Lys	Pro	Gln 500	Ile	Thr	Val	Gln	Pro 505	Glu	Thr	Gln	Ser	Ala 510
Ile	Lys	Gly	Ser	Asn 515	Leu	Ser	Phe	Ile	Cys 520	Ser	Ala	Ala	Ser	Ser 525
Ser	Asp	Ser	Pro	Met 530	Thr	Phe	Ala	Trp	Lys 535	Lys	Asp	Asn	Glu	Leu 540
Leu	His	Asp	Ala	Glu 545	Met	Glu	Asn	Tyr	Ala 550	His	Leu	Arg	Ala	Gln 555
Gly	Gly	Glu	Val	Met 560	Glu	Tyr	Thr	Thr	Ile 565	Leu	Arg	Leu	Arg	Glu 570
Val	Glu	Phe	Ala	Ser 575	Glu	Gly	Lys	Tyr	Gln 580	Сув	Val	Ile	Ser	Asn 585
His	Phe	Gly	Ser	Ser 590	Tyr	Ser	Val	Lys	Ala 595	Lys	Leu	Thr	Val	Asn 600
				605					610				Ile	615
				620					625				His	630
Ala	Pro	Gln	Ile	Ala 635	Trp	Gln	Lys	Asp	Gly 640	Gly	Thr	Asp	Phe	Pro 645
				650					655				Asp	660
				665					670				Tyr	675
Cys	Thr	Ala	Gln	Asn 680	Ser	Ala	Gly	Ser	Ile 685		Ala	. Asn	Ala	Thr 690
				695					700					Asp 705
				710					715					Ala 720
_				725					730	1				Ser 735
Pro	Leu	Val	Val	Thr 740		Arg	η His	Phe	Phe 745		Ala	Gly	Asn	750

Leu	Leu	Ile	Ile	Val 755	Asp	Ser	Asp	Val	Ser 760	Asp	Ala	Gly	Lys	Tyr 765
Thr	Cys	Glu	Met	Ser 770	Asn	Thr	Leu	Gly	Thr 775	Glu	Arg	Gly	Asn	Val 780
Arg	Leu	Ser	Val	Ile 785	Pro	Thr	Pro	Thr	Cys 790	Asp	Ser	Pro	Gln	Met 795
Thr	Ala	Pro	Ser	Leu 800	Asp	Asp	Asp	Gly	Trp 805	Ala	Thr	Val	Gly	Val 810
Val	Ile	Ile	Ala	Val 815	Val	Сув	Cys	Val	Val 820	Gly	Thr	Ser	Leu	Val 825
Trp	Val	Val	Ile	Ile 830	Tyr	His	Thr	Arg	Arg 835	Arg	Asn	Glu	Asp	Cys 840
Ser	Ile	Thr	Asn	Thr 845	Asp	Glu	Thr	Asn	Leu 850	Pro	Ala	Asp	Ile	Pro 855
Ser	Tyr	Leu	Ser	Ser 860	Gln	Gly	Thr	Leu	Ala 865	Asp	Arg	Gln	Asp	Gly 870
Tyr	Val	Ser	Ser	Glu 875		Gly	Ser	His	His 880	Gln	Phe	Val	Thr	Ser 885
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Cys	His	Ile	Asp	Asn 905		Ser	Glu	Ala	Asp 910		Glu	. Ala	Ala	Thr 915
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Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met

95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met 110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met 125 130 130

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Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg

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C1-	. cl	, TT++	Leu			Ç∆*	בול י				Pro	Glv	Glv	

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Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg 80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala

				95					100					105
Val	Leu	Thr	Ser	Arg 110	Ala	Thr	Leu	Ser	Thr 115	Leu	Ala	Val	Ala	Val 120
Asn	Arg	Thr	Val	Ala 125	His	His	Phe	Pro	Arg 130	Leu	Leu	Tyr	Phe	Thr 135
Gly	Gln	Arg	Gly	Ala 140	Arg	Ala	Pro	Ala	Gly 145	Met	Gln	Val	Val	Ser 150
His	Gly	Asp	Glu	Arg 155	Pro	Ala	Trp	Leu	Met 160	Ser	Glu	Thr	Leu	Arg 165
His	Leu	His	Thr	His 170	Phe	Gly	Ala	Asp	Tyr 175	Asp	Trp	Phe	Phe	Ile 180
Met	Gln	Asp	Asp	Thr 185	Tyr	Val	Gln	Ala	Pro 190	Arg	Leu	Ala	Ala	Leu 195
Ala	Gly	His	Leu	Ser 200	Ile	Asn	Gln	Asp	Leu 205	Tyr	Leu	Gly	Arg	Ala 210
Glu	Glu	Phe	Ile	Gly 215	Ala	Gly	Glu	Gln	Ala 220	Arg	Tyr	Cys	His	Gly 225
Gly	Phe	Gly	Tyr	Leu 230	Leu	Ser	Arg	Ser	Leu 235	Leu	Leu	Arg	Leu	Arg 240
Pro	His	Leu	Asp	Gly 245	Cys	Arg	Gly	Asp	Ile 250	Leu	Ser	Ala	Arg	Pro 255
Asp	Glu	Trp	Leu	Gly 260	Arg	Cys	Leu	Ile	Asp 265	Ser	Leu	Gly	Val	Gly 270
Cys	Val	Ser	Gln	His 275		Gly	Gln	Gln	Tyr 280		Ser	Phe	Glu	Leu 285
Ala	Lys	Asn	Arg	Asp 290		Glu	Lys	Glu	Gly 295		Ser	Ala	Phe	Leu 300
Ser	Ala	Phe	Ala	Val 305		Pro	Val	Ser	Glu 310		Thr	Leu	Met	Tyr 315
Arg	Leu	His	Lys	Arg 320		Ser	Ala	Leu	Glu 325		Glu	Arg	Ala	Tyr 330
Ser	Glu	Ile	Glu	Gln 335		Gln	Ala	Gln	11e 340		Asn	. Leu	Thr	Val 345
Leu	Thr	Pro	Glu	Gly 350		Ala	Gly	Leu	Ser 355		Pro	Val	. Gly	Leu 360

Pro	Ala	Pro	Phe	Thr 365	Pro	His	Ser	Arg	Phe 370	Glu	Val	Leu	Gly	Trp 375
Asp	Tyr	Phe	Thr	Glu 380	Gln	His	Thr	Phe	Ser 385	Cys	Ala	Asp	Gly	Ala 390
Pro	Lys	Cys	Pro	Leu 395	Gln	Gly	Ala	Ser	Arg 400	Ala	Asp	Val	Gly	Asp 405
Ala	Leu	Glu	Thr	Ala 410	Leu	Glu	Gln	Leu	Asn 415	Arg	Arg	Tyr	Gln	Pro 420
Arg	Leu	Arg	Phe	Gln 425	Lys	Gln	Arg	Leu	Leu 430	Asn	Gly	Tyr	Arg	Arg 435
Phe	Asp	Pro	Ala	Arg 440	Gly	Met	Glu	Tyr	Thr 445	Leu	qaA	Leu	Leu	Leu 450
Glu	Cys	Val	Thr	Gln 455	Arg	Gly	His	Arg	Arg 460	Ala	Leu	Ala	Arg	Arg 465
Val	Ser	Leu	Leu	Arg 470	Pro	Leu	Ser	Arg	Val 475	Glu	Ile	Leu	Pro	Met 480
Pro	Tyr	Val	Thr	Glu 485	Ala	Thr	Arg	Val	Gln 490	Leu	Val	Leu	Pro	Leu 495
Leu	Val	Ala	Glu	Ala 500	Ala	Ala	Ala	Pro	Ala 505	Phe	Leu	Glu	Ala	Phe 510
Ala	Ala	Asn	Val	Leu 515	Glu	Pro	Arg	Glu	His 520	Ala	Leu	Leu	Thr	Leu 525
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Pro	Phe	Leu	. Gly	Val 545		Ala	. Ala	Ala	Ala 550		Leu	Glu	Arg	Arg 555
Tyr	Pro	Gly	Thr	Arg 560		ı Ala	Trp	Leu	Ala 565	. Val	Arg	Ala	Glu	Ala 570
			val	575	•				580					585
Val	. Asp	Thr	Leu	Phe 590		e Leu	ı Thr	Thr	Val 595		Thr	Arg	Pro	Gly 600
Pro	Glu	ı Val	. Leu	Asn 605		g Cys	s Arg	, Met	. Asr 610		ılle	Ser	Gly	Trp 615
Glr	n Ala	a Phe	e Phe	Pro		l His	s Phe	e Gln	Glu 625		e Asn	Pro	Ala	Leu 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile 650 655 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr 670 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met 700 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val 715 710 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro 725 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu 755 765 Gln Glu Gln Ala Asn Ser Thr 770

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<211> 1572

<212> DNA

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tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
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ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

gtttgagtca attaatatgg acacaaatga catgtggtta atgatgagaa 450 aagcttacaa atacgccttt gataagtata gagaccaata caactggttc 500 tteettgeae geeceactae gtttgetate attgaaaaee taaagtattt 550 tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600 aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650 gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700 tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750 cagtttgcct gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800 gatggaaaag atgtatttaa taccaaatct gttgggcttt ctattaaaga 850 ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900 tggctgttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950 tatggggtat accgccttag ggcatttggg catattttca atgatgcatt 1000 ggttttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050 agcgtgaata tgatctttgt ataggacgtg tgttgtcatt atttgtagta 1100 gtaactacat atccaataca gctgtatgtt tctttttctt ttctaatttg 1150 gtggcactgg tataaccaca cattaaagtc agtagtacat ttttaaatga 1200 gggtggtttt tttctttaaa acacatgaac attgtaaatg tgttggaaag 1250 aagtgtttta agaataataa ttttgcaaat aaactattaa taaatattat 1300 atgtgataaa ttctaaatta tgaacattag aaatctgtgg ggcacatatt 1350 tttgctgatt ggttaaaaaa ttttaacagg tctttagcgt tctaagatat 1400 gcaaatgata tetetagttg tgaatttgtg attaaagtaa aaettttage 1450 tgtgtgttcc ctttacttct aatactgatt tatgttctaa gcctccccaa 1500 gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550 attaaagtga aagttgaaaa at 1572

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Gly	His	Gly	Asn	Arg 35	Met	His	His	His	Glu 40	His	His	His	Leu	Gln 45
Ala	Pro	Asn	Lys	Glu 50	Asp	Ile	Leu	Lys	Ile 55	Ser	Glu	Asp	Glu	Arg 60
Met	Glu	Leu	Ser	Lys 65	Ser	Phe	Arg	Val	Tyr 70	Cys	Ile	Ile	Leu	Val 75
Lys	Pro	Lys	Asp	Val 80	Ser	Leu	Trp	Ala	Ala 85	Val	Lys	Glu	Thr	Trp 90
Thr	Lys	His	Cys	Asp 95	Lys	Ala	Glu	Phe	Phe 100	Ser	Ser	Glu	Asn	Val 105
Lys	Val	Phe	Glu	Ser 110	Ile	Asn	Met	Asp	Thr 115	Asn	Asp	Met	Trp	Leu 120
Met	Met	Arg	Lys	Ala 125	Tyr	Lys	Tyr	Ala	Phe 130	Asp	Lys	Tyr	Arg	Asp 135
Gln	Tyr	Asn	Trp	Phe 140	Phe	Leu	Ala	Arg	Pro 145	Thr	Thr	Phe	Ala	Ile 150
Ile	Glu	Asn	Leu	Lys 155	Tyr	Phe	Leu	Leu	Lys 160		Asp	Pro	Ser	Gln 165
Pro	Phe	Tyr	Leu	Gly 170		Thr	Ile	Lys	Ser 175		Asp	Leu	Glu	Tyr 180
Val	Gly	Met	Glu	Gly 185		Ile	Val	Leu	Ser 190		Glu	Ser	Met	Lys 195
Arg	, Leu	Asn	Ser	Leu 200		Asn	Ile	Pro	Glu 205	Lys ;	Cys	Pro	Glu	Gln 210
GlΣ	gly	Met	. Ile	215		Ile	Ser	Glu	220	Lys	Gln	Leu	. Ala	. Val 225
Cys	. Leu	Lys	. Tyr	230		Val	. Phe	ala	Glu 235		n Ala	Glu	Asp	Ala 240
Asp	Gly	Lys	s Asp	Val 245		. Asr	Thr	Lys	Ser 250		. Gly	r Leu	. Ser	255
T + r	. (1)	, 7 ₁ =	Mat	· Thr	- ጥላታ	His	Pro	Asr	Glr	ı Val	Val	. Glu	ı Gly	y Cys

270

315

260 265 Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln 280 275 Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly 295 His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser 310 Asp Asn Asp <210> 342 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 342 tccccaagcc gttctagacg cgg 23 <210> 343 <211> 18 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 343 ctggttcttc cttgcacg 18 <210> 344 <211> 28 <212> DNA <213> Artificial Sequence <223> Synthetic Oligonucleotide Probe <400> 344 gcccaaatgc cctaaggcgg tatacccc 28 <210> 345 <211> 50 <212 > DNA <213 > Artificial Sequence <220>

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<400> 347
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atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250
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 ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350
gaactgggaa tattttcaat ccagctgcta cttctttct actgacacca 400
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taaaatgaga gagttttta ttggactgtc agaccaggtt gtcgagggtc 550
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gatgtagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
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<211> 219

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<213> Homo Sapien

<400> 377

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1 5 10 15

Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro $20 \hspace{1cm} 25 \hspace{1cm} 30$

Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser 80 · 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu 95 100 105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser 110 115 120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg 125 130 135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp 140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala 170 175 180

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Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
                                     190
                 185
Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
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                                      205
Asn Pro Leu Asn Lys Gly Lys Ser Leu
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35 40 45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
50 55 60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly 80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val 95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg 110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val 125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
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His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu 170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe 185 190 195

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Leu	Ala	Leu	Ile	Thr 260	Leu	Gly	Ile	Cys	Cys 265	Ala	Tyr	Arg	Arg	Gly 270
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
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Gly	Lys	Pro	Asp	Gly 290	Val	Asn	Tyr	Ile	Arg 295	Thr	Asp	Glu	Glu	Gly 300
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